
Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: markspencer

Timestamp: Wed Jun 27 06:52:47 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: Version No: 10584082 1.0

Input Set:

Output Set:

Started: 2007-06-21 15:58:53.503 Finished:

2007-06-21 15:58:55.725

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 222 ms

Total Warnings: 40 Total Errors: 6

No. of SeqIDs Defined: 46

> Actual SeqID Count: 46

Err	or code	Error Descript	ion								
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(7)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(8)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(9)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(10)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(11)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(12)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(13)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(14)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(15)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(16)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(17)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(18)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(20)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(21)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(22)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(23)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(24)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(25)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(26)

Input Set:

Output Set:

Started: 2007-06-21 15:58:53.503 **Finished:** 2007-06-21 15:58:55.725

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 222 ms

Total Warnings: 40

Total Errors: 6

No. of SeqIDs Defined: 46

Actual SeqID Count: 46

Error code		Error Description
		This error has occured more than 20 times, will not be displayed
E	257	Invalid sequence data feature in <221> in SEQ ID (37)
E	257	Invalid sequence data feature in <221> in SEQ ID (41)
E	257	Invalid sequence data feature in <221> in SEQ ID (41)
E	257	Invalid sequence data feature in <221> in SEQ ID (42)
E	257	Invalid sequence data feature in <221> in SEQ ID (42)
E	257	Invalid sequence data feature in <221> in SEQ ID (42)

SEQUENCE LISTING

```
<110> OHYAMA, KANJI
<120> MARCHANTIALES-DERIVED UNSATURATED FATTY ACID SYNTHETASE
     GENES AND USE OF THE SAME
<130> 47236-0009-00-US
<140> 10584082
<141> 2007-06-21
<150> 10/584,082
<151> 2006-06-22
<150> PCT/JP04/19196
<151> 2004-12-22
<150> JP 2003-425673
<151> 2003-12-22
<160> 46
<170> PatentIn Ver. 3.3
<210> 1
<211> 2519
<212> DNA
<213> Marchantia polymorpha
<220>
<221> CDS
<222> (253)..(1698)
<400> 1
atagatccaa tttcataagt cgacgagaaa ggcagaaggc gagaagcggc aggcagcgag 60
egegagegee agagetettg eteceetege teategeteg eattgeegea tittgtgagt 120
gtcggactga tcactcagtc cgtcactgca aacgcgagcg agcgagagtg cgagtgagcg 180
agcgagcgag cgagagccgc ggtgtgtctg tgagatccaa tcctttttct gctttgcgcg 240
ctgtggggcg cg atg gcc tcg tcc acc acc gcc gtg aag caa tct tcg 291
             Met Ala Ser Ser Thr Thr Thr Ala Val Lys Gln Ser Ser
ggt ggg ctg tgg tcg aaa tgg ggc acc ggc agc aac ttg agc ttc gtg 339
Gly Gly Leu Trp Ser Lys Trp Gly Thr Gly Ser Asn Leu Ser Phe Val
    15
                        20
teg ege aag gag eag eag eag eag eag eag age tet eee gag geg
Ser Arg Lys Glu Gln Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala
                    35
30
                                        40
                                                             45
tcg act ccc gcg gcg cag cag gag aaa tcc atc agt aga gaa tcc atc
                                                                  435
```

Ser Thr Pro Ala Ala Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile

50 55 60

		ggc Gly		_						_	-		-		-	483
_	-	tgc Cys 80			-			_	_			-		_	_	531
		aag Lys	_		_							_	_	-		579
_	_	gcc Ala	_	_			_	_				_	_			627
_		ctc Leu	_	_	_				_	_			_			675
	_	gag Glu	_		_	_		_	-	_		_			_	723
_		cag Gln 160			_	_	-		_					_	-	771
_		aat Asn		-			_	_	-		_	-				819
_	_	acg Thr		_		_	_	_		_		_	_	_		867
		cag Gln		-				_		-					-	915
, ,		gag Glu		_	_			_					_		2.2	963
		ttc Phe 240	_	_			_					_		_		1011
		cac His			-	_		-	-	-	_	_		_		1059
	-	ccc Pro	_		-				_		_		_	_	-	1107

	_	_		_	-	gac Asp				_	_			_		1155
_			_			ccg Pro				_	-	-		_		1203
_		_	_		-	cac His	_	-				_				1251
_	-				_	gcc Ala 340	_							-		1299
		-	_			att Ile	_				_	-		_		1347
		-	-		-	ttt Phe	-		-	-		-		-		1395
		_				atg Met	_				_			-		1443
	_	-		-		tcg Ser		-			-					1491
	-					ggc Gly 420	_			_					-	1539
	_			_		cac His			_	_	_				_	1587
_			_	-	_	cac His		_			-	-	_	-	-	1635
	_		-	_	_	gtc Val					-		-	-		1683
-		aaa Lys 480	-	tag	atco	gacga	aga q	gttt	ccad	cc aa	acaca	agtta	a gaa	acaaq	ggga	1738
ataç	gtaco	gag a	agaaq	ggaga	ac aq	gcaad	cctg	g act	tttt	igtt	cct	gatgt	itg (catad	ctttct	1798

cgaatatacg tctccacgcc ttcaagtttc agcttcaact gattgtcttc agtaaccatc 1858

gettgetcca actgggegae etgeagaatt gaagateagt titactgagt tigtacegag 1918
agtiteccaa attitgitgi aggetgatga eccaateeta geatacaett taggaataag 1978
cagteteaac ataattaggi ecateattea geaattiega tacagegeet gggateegae 2038
gagtitacae gatgagtatg getigtaaet ggeetietea aggiageeti ggateteece 2098
gggeetettig ecateceatt eaceeaateg agatietigea gieteeaaee tittetggaa 2158
gitteteaate tigtaacetet gittgiagaga tageataege eacaagaeaa ggietitigti 2218
aacacagteg tetaacaaac ageaagitigt giggatigge atetaaataa eegeetetigg 2278
teaagiaaca geaggitte egeagitiee aggaacatae tittgitietig teacageeag 2338
geggitgaata giaaageeaa tieaacaeat aegggagaag atgggiegat attigtatit 2398
ggeagggitgi eeagatitea eeeateagie teteaetige tigtaaaaaa aaaaaaaaa 2518
teaaaattit gegegggaa teateaata aettaeeatt tigtaaaaaa aaaaaaaaa 2518
a

<210> 2

<211> 481

<212> PRT

<213> Marchantia polymorpha

<400> 2

Met Ala Ser Ser Thr Thr Ala Val Lys Gln Ser Ser Gly Gly Leu

1 10 15

Trp Ser Lys Trp Gly Thr Gly Ser Asn Leu Ser Phe Val Ser Arg Lys 20 25 30

Glu Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala Ser Thr Pro 35 40 45

Ala Ala Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile Pro Glu Gly
50 55 60

Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro Ser Asp Cys
65 70 75 80

Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala Phe Gly Lys
85 90 95

Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly Arg Asp Ala 100 105 110

Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp Gln Phe Leu 115 120 125

Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro Val Ser Glu 130 135 140

Leu 145	Val	Lys	Asp	Tyr	Arg 150	Asp	Leu	Arg	Thr	Ala 155	Phe	Met	Arg	Ser	Gln 160
Leu	Phe	Lys	Ser	Ser 165	Lys	Met	Tyr	Tyr	Val 170	Thr	Lys	Суз	Val	Thr 175	Asn
Phe	Ala	Ile	Leu 180	Ala	Ala	Ser	Leu	Ala 185	Val	Ile	Ala	Trp	Ser 190	Gln	Thr
Tyr	Leu	Ala 195	Val	Leu	Суз	Ser	Ser 200	Phe	Leu	Leu	Ala	Leu 205	Phe	Trp	Gln
Gln	Cys 210	Gly	Trp	Leu	Ser	His 215	Asp	Phe	Leu	His	His 220	Gln	Val	Thr	Glu
Asn 225	Arg	Ser	Leu	Asn	Thr 230	Tyr	Phe	Gly	Gly	Leu 235	Phe	Trp	Gly	Asn	Phe 240
Ala	Gln	Gly	Tyr	Ser 245	Val	Gly	Trp	Trp	Lys 250	Thr	Lys	His	Asn	Val 255	His
His	Ala	Ala	Thr 260	Asn	Glu	Cys	Asp	Asp 265	Lys	Tyr	Gln	Pro	Ile 270	Asp	Pro
Asp	Ile	Asp 275	Thr	Val	Pro	Leu	Leu 280	Ala	Trp	Ser	Lys	Glu 285	Ile	Leu	Ala
Thr	Val 290	Asp	Asp	Gln	Phe	Phe 295	Arg	Ser	Ile	Ile	Ser 300	Val	Gln	His	Leu
Leu 305	Phe	Phe	Pro	Leu	10 Jeu	Phe	Leu	Ala	Arg	Phe 315	Ser	Trp	Leu	His	320
	Trp			325					330		_	-		335	-
	Glu		340					345	_	_			350	_	
	Phe	355					360				-	365			
	Gln 370			-	-	375					380				
385	Asn	_		_	390			_		395					400
	Val			405					410					415	_
	Thr	_	420					425					430		
ьеи	Pro	Arg	птЗ	ASN	ьeu	АІА	Lys	val	АІА	LIO	пта	val 445	туѕ	мта	ьeu

450 455 Val Cys Arg Val Phe Asn Arg Leu Val Glu Val Ala Tyr Ala Ala Lys 465 470 475 480 Val <210> 3 <211> 1577 <212> DNA <213> Marchantia polymorpha <220> <221> CDS <222> (194)..(1066) <400> 3 ctcaacgctc tetetegecc geeetetgtc ttcegetgeg cettettetc ggegeetett 60 tetgtegaga ggageggeag etgeagetet egagagaggg gageaggaeg agagegaggg 120 cgaatccgcc gagagtcgat cgggattggg tagaaggagg agaaggagga gaagaggagg 180 aggaggagca gcg atg gag gcg tac gag atg gtg gat agt ttt gtg tcg 229 Met Glu Ala Tyr Glu Met Val Asp Ser Phe Val Ser aag acg gtt ttc gaa acg ctg cag aga ctg agg ggc gga gtc gtg ttg 277 Lys Thr Val Phe Glu Thr Leu Gln Arg Leu Arg Gly Gly Val Val Leu 15 2.0 2.5 acg gaa tot gog ato acc aaa ggt ttg coa tgo gto gat ago cog acg 325 Thr Glu Ser Ala Ile Thr Lys Gly Leu Pro Cys Val Asp Ser Pro Thr 30 35 ccg atc gtt ctt ggg ttg tcg tcc tac ttg aca ttc gtg ttt ctc ggg 373 Pro Ile Val Leu Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly 45 50 55 ctc att gtc atc aag agc ctg gat ctt aag ccc cgc tcc aag gag ccc 421 Leu Ile Val Ile Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro 65 gcc att ttg aac ctg ttt gtg atc ttc cac aac ttc gtc tgc ttc gca 469 Ala Ile Leu Asn Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala 85 ctc agt ctg tac atg tgc gtg gga att gtc cgt caa gct atc ctc aac 517 Leu Ser Leu Tyr Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn 95 100 105 agg tac tct ctg tgg ggc aat gcg tac aat ccc aaa gaa gtt caa atg 565 Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met

Cys Ala Lys His Gly Leu His Tyr Glu Glu Leu Ser Leu Gly Thr Gly

110 115 120

ggc cac ctg ctc tac att ttc tac atg tca aag tac atc gag ttt atg Gly His Leu Leu Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met 125 130 135 140	3
gac acg gtc att atg att ttg aag cgc aac acg cgc cag atc act gtg 661 Asp Thr Val Ile Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val 145 150 155	-
ttg cat gtg tac cac cac gca tcc atc tcc ttc atc tgg tgg atc atc 709 Leu His Val Tyr His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile 160 165 170	•
gee tae cat get eet gge ggt gaa get tat tte tet gee gea ttg aac 757 Ala Tyr His Ala Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn 175 180 185	7
tcc gga gta cat gtg ctc atg tac ctc tac tac ctt ttg gca gca act 805 Ser Gly Val His Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr 190 195 200	ò
ctg gga aag aac gag aaa gct cgc cgc aag tac cta tgg tgg gga aaa 853 Leu Gly Lys Asn Glu Lys Ala Arg Arg Lys Tyr Leu Trp Trp Gly Lys 205 210 215 220	3
tac ttg aca cag ctg cag atg ttc cag ttt gtc ctt aac atg att cag 901 Tyr Leu Thr Gln Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln 225 230 235	-
gct tac tac gat att aag aac aac tcg cct tac cca caa ttt ttg atc 949 Ala Tyr Tyr Asp Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile 240 245 250	•
cag att ttg ttc tac tac atg atc tcg ctt tta gcg cta ttt gga aac 997 Gln Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn 255 260 265	7
ttt tac gtt cac aaa tac gta tca gcg ccc gca aaa cct gcg aag atc Phe Tyr Val His Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile 270 275 280	15
aag agc aaa aag gca gaa taa gacaccaccc tagtgacaag aagattttac 109 Lys Ser Lys Lys Ala Glu 285 290	96
actaaactgt agttttagca cccatcgttg acacgaatac attctggttc tgcctgtctt 115	6
ggaagagteg aageatteag gageteteee gtteeatega teaaaetegg aacgaagtge 121	. 6
accttttage tgcgatgaga gtetttaett eetgageegt egttettgat gtggtetgta 127	16
geteageeat aegtgtagea tagetggaae atetggettt teaggaaagt eggeaaggea 133	36
agaattcgac ccttgaacta gacaaggttc tgctgattca gcaaccatta gtgagtcact 139)6
ggttaacaaa atcacagttt tgggccctta gttagtgaca accaacccta acactttgat 145	6

acacgagtta tcgttcgcga gtggaagtgt aaaaatgtgc tttcccaatc atcttgagtt 1516
ggttcctttt gaagtaaagg aaaattctat gattgttgag tccaaaaaaa aaaaaaaaa 1576
a 1577

<210> 4

<211> 290

<212> PRT

<213> Marchantia polymorpha

<400> 4

Met Glu Ala Tyr Glu Met Val Asp Ser Phe Val Ser Lys Thr Val Phe 1 5 10 15

Glu Thr Leu Gln Arg Leu Arg Gly Gly Val Val Leu Thr Glu Ser Ala 20 25 30

Ile Thr Lys Gly L